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RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/09/844,268

TIME: 11:28:19

Input Set : N:\Crf3\RULE60\09844268.raw

Output Set: N:\CRF3\01282002\I844268.raw

1 <110> APPLICANT: BOSWORTH, BRAD
2 VOGELI, PETER
3 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS TO IDENTIFY SWINE GENETICALLY
4 RESISTANT TO F18 E. COLI ASSOCIATED DISEASES
5 <130> FILE REFERENCE: 21419/90368
6 <140> CURRENT APPLICATION NUMBER: 09/844,268
7 <141> CURRENT FILING DATE: 2001-04-27
8 <150> PRIOR APPLICATION NUMBER: 09/443,766
9 <151> PRIOR FILING DATE: 1999-11-19
12 <160> NUMBER OF SEQ ID NOS: 13
13 <170> SOFTWARE: PatentIn Ver. 2.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 20
17 <212> TYPE: DNA
18 <213> ORGANISM: Artificial Sequence
19 <220> FEATURE:
20 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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33 <210> SEQ ID NO: 3
34 <211> LENGTH: 22
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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44 <212> TYPE: DNA
45 <213> ORGANISM: Artificial Sequence
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47 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
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67     ctgcctgaac gtctatcaag atc 23
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70 <211> LENGTH: 22
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
73 <220> FEATURE:
74 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
75 <400> SEQUENCE: 7
76     agagtttctt catgcccaca gg 22
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79 <211> LENGTH: 22
80 <212> TYPE: DNA
81 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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85     ctgctacagg accaccagca tc 22
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88 <211> LENGTH: 35
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
91 <220> FEATURE:
92 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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94     accagcagcg caaagtcctt gacgggcacg gcctc 35
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98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial Sequence
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101 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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103     ctccctgtgc cttggaagtg at 22
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106 <211> LENGTH: 22
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110 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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115 <211> LENGTH: 1269
116 <212> TYPE: DNA
117 <213> ORGANISM: Porcine
118 <220> FEATURE:
119 <221> NAME/KEY: CDS
120 <222> LOCATION: (9)..(1103)
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124      1          5          10
125      cta gtc tgt gtt tta gca gca att ttc ttc ctg aac gtc tat caa gac 98
126      Leu Val Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp
127      15          20          25          30
128      ctc ttt tac agt ggc tta gac ctg ctg gcc ctg tgt cca gac cat aac 146
129      Leu Phe Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn
130      35          40          45
131      gtg gta tca tct ccc gtg gcc ata ttc tgc ctg gcg ggc acg ccg gta 194
132      Val Val Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val
133      50          55          60
134      cac ccc aac gcc tcc gat tcc tgt ccc aag cat cct gcc tcc ttt tcc 242
135      His Pro Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser
136      65          70          75
137      ggg acc tgg act att tac ccg gat ggc cgg ttt ggg aac cag atg gga 290
138      Gly Thr Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly
139      80          85          90
140      cag tat gcc acg ctg ctg gcc ctg gcg cag ctc aac ggc cgc cag gcc 338
141      Gln Tyr Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala
142      95          100          105          110
143      ttc atc cag cct gcc atg cac gcc gtc ctg gcc ccc gtg ttc cgc atc 386
144      Phe Ile Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile
145      115          120          125
146      acg ctg cct gtc ctg gcg ccc gag gta gac agg cac gct cct tgg cgg 434
147      Thr Leu Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg
148      130          135          140
149      gag ctg gag ett cac gac tgg atg tcc gag gat tat gcc cac tta aag 482
150      Glu Leu Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys
151      145          150          155
152      gag ccc tgg ctg aag ctc acc ggc ttc ccc tgc tcc tgg acc ttc ttc 530
153      Glu Pro Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe
154      160          165          170
155      cac cac ctc cgg gag cag atc cgc agc gag ttc acc ctg cac gac cac 578

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156   His His Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His
157   175                               180                               185                               190
158   ctt cgg caa gag gcc cag ggg gta ctg agt cag ttc cgt cta ccc cgc      626
159   Leu Arg Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg
160                               195                               200                               205
161   aca ggg gac cgc ccc agc acc ttc gtg ggg gtc cac gtg cgc cgc ggg      674
162   Thr Gly Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly
163                               210                               215                               220
164   gac tat ctg cgt gtg atg ccc aag cgc tgg aag ggg gtg gtg ggt gac      722
165   Asp Tyr Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp
166                               225                               230                               235
167   ggc cgt tac ctc cag cag gct atg gac tgg ttc cgg gcc cga tac gaa      770
168   Gly Arg Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu
169                               240                               245                               250
170   gcc ccc gtc ttt gtg gtc acc agc aac ggc atg gag tgg tgc cgg aag      818
171   Ala Pro Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys
172   255                               260                               265                               270
173   aac atc gac acc tcc cgg ggg gac gtg atc ttt gct ggc gat ggg cgg      866
174   Asn Ile Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg
175                               275                               280                               285
176   gag gcc gcg ccc gcc agg gac ttt gcg ctg ctg gtg cag tgc aac cac      914
177   Glu Ala Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His
178                               290                               295                               300
179   acc atc atg acc att ggc acc ttc ggc ttc tgg gcc gcc tac ctg gct      962
180   Thr Ile Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala
181                               305                               310                               315
182   ggt gga gat acc atc tac ttg gct aac ttc acc ctg ccc act tcc agc      1010
183   Gly Gly Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser
184   320                               325                               330
185   ttc ctg aag atc ttt aaa ccc gag gct gcc ttc ctg ccc gag tgg gtg      1058
186   Phe Leu Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val
187   335                               340                               345                               350
188   ggc att aat gca gac ttg tct cca ctc cag atg ttg gct ggg cct      1103
189   Gly Ile Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
190                               355                               360                               365
191   tgaaccagcc aggagccttt ctggaatagc ctgggtcaac ccagggccag cgttatgggt 1163
192   ctccggaagc ccgagtaact tccggagatg ctgggtggtcc tgtagcaggc tggacactta 1223
193   tttcaagagt gattctaatt ggctggactc agaggaaacc ctgcag      1269
195 <210> SEQ ID NO: 13
196 <211> LENGTH: 365
197 <212> TYPE: PRT
198 <213> ORGANISM: Porcine
199 <400> SEQUENCE: 13
200   Met Trp Val Pro Ser Arg Arg His Leu Cys Leu Thr Phe Leu Leu Val
201       1                               5                               10                               15
202   Cys Val Leu Ala Ala Ile Phe Phe Leu Asn Val Tyr Gln Asp Leu Phe
203                               20                               25                               30
204   Tyr Ser Gly Leu Asp Leu Leu Ala Leu Cys Pro Asp His Asn Val Val
205       35                               40                               45

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206   Ser Ser Pro Val Ala Ile Phe Cys Leu Ala Gly Thr Pro Val His Pro
207       50                      55                      60
208   Asn Ala Ser Asp Ser Cys Pro Lys His Pro Ala Ser Phe Ser Gly Thr
209       65                      70                      75                      80
210   Trp Thr Ile Tyr Pro Asp Gly Arg Phe Gly Asn Gln Met Gly Gln Tyr
211                      85                      90                      95
212   Ala Thr Leu Leu Ala Leu Ala Gln Leu Asn Gly Arg Gln Ala Phe Ile
213                      100                      105                      110
214   Gln Pro Ala Met His Ala Val Leu Ala Pro Val Phe Arg Ile Thr Leu
215                      115                      120                      125
216   Pro Val Leu Ala Pro Glu Val Asp Arg His Ala Pro Trp Arg Glu Leu
217                      130                      135                      140
218   Glu Leu His Asp Trp Met Ser Glu Asp Tyr Ala His Leu Lys Glu Pro
219                      145                      150                      155                      160
220   Trp Leu Lys Leu Thr Gly Phe Pro Cys Ser Trp Thr Phe Phe His His
221                      165                      170                      175
222   Leu Arg Glu Gln Ile Arg Ser Glu Phe Thr Leu His Asp His Leu Arg
223                      180                      185                      190
224   Gln Glu Ala Gln Gly Val Leu Ser Gln Phe Arg Leu Pro Arg Thr Gly
225                      195                      200                      205
226   Asp Arg Pro Ser Thr Phe Val Gly Val His Val Arg Arg Gly Asp Tyr
227                      210                      215                      220
228   Leu Arg Val Met Pro Lys Arg Trp Lys Gly Val Val Gly Asp Gly Arg
229                      225                      230                      235                      240
230   Tyr Leu Gln Gln Ala Met Asp Trp Phe Arg Ala Arg Tyr Glu Ala Pro
231                      245                      250                      255
232   Val Phe Val Val Thr Ser Asn Gly Met Glu Trp Cys Arg Lys Asn Ile
233                      260                      265                      270
234   Asp Thr Ser Arg Gly Asp Val Ile Phe Ala Gly Asp Gly Arg Glu Ala
235                      275                      280                      285
236   Ala Pro Ala Arg Asp Phe Ala Leu Leu Val Gln Cys Asn His Thr Ile
237                      290                      295                      300
238   Met Thr Ile Gly Thr Phe Gly Phe Trp Ala Ala Tyr Leu Ala Gly Gly
239                      305                      310                      315                      320
240   Asp Thr Ile Tyr Leu Ala Asn Phe Thr Leu Pro Thr Ser Ser Phe Leu
241                      325                      330                      335
242   Lys Ile Phe Lys Pro Glu Ala Ala Phe Leu Pro Glu Trp Val Gly Ile
243                      340                      345                      350
244   Asn Ala Asp Leu Ser Pro Leu Gln Met Leu Ala Gly Pro
245                      355                      360                      365

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